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NAMRU-6 Studies Fever to Predict Pandemics in Developing Countries

Filed under Public Health, Research and development {no comments}



Dengue is a mosquito-borne viral disease transmitted by female mosquitoes of the species Aedes aegypti.

LIMA, Peru – Navy Medicine researchers recently published a study reporting for the first time how fever affects mobility during an outbreak of a mosquito-borne pathogen like dengue. The study was published in the *Proceedings of the Royal Society B: Biological Sciences*.

The U.S. Naval Medical Research Unit No. 6 (NAMRU-6), in collaboration with several U.S. universities, studies the transmission dynamics of dengue virus in residents living in the Amazonian city of Iquitos, Peru. The primary importance of these findings is to support mathematical models of dengue virus transmission. Cohort studies of this stature and magnitude only exist in two other locations and have provided critical background information for vaccine deployment and vector control intervention trials.

"Human mobility is an important driver of (disease) transmission dynamics. Mobility increases potential contact in locations where vectors (mosquitoes) are present and enhances transmission and spread of the disease," said Amy Morrison, program manager and science advisor at the lab. "When study volunteers are diagnosed with dengue we ask them to let us evaluate them clinically throughout their illness, to carry GPS units to track their movements, and to answer questions about symptoms and personal activities. We also collect mosquitoes in their homes."

The GPS data showed people with fevers spent more time in their homes, but visit more locations with a far less predictable routine than their U.S. counterparts; an observation the disease modelers suggest enhances disease transmission, according to Morrison.

The majority of dengue infections are mild or asymptomatic, a characteristic shared by the Zika virus. NAMRU-6 researchers are interested in determining the role of how this "majority" of infections are transmitted. Morrison went on to explain the research team compared the movement of people with and without fevers and was able to quantify the impact of fever on movement patterns, and how these observations would affect dengue transmission

"Conventional wisdom tells us people with more symptoms have more virus in their blood and would be better at infecting mosquitoes. Our fever studies indicate people with fevers move less than we would expect from someone without symptoms," said Morrison. "Our hypothesis is – even though asymptomatic and mild cases

may be less efficient at infecting mosquitoes, asymptomatic people are spreading the virus more quickly to more locations and have higher numbers than symptomatic cases. Asymptomatic cases may account for far more of the disease transmission. Because current control measures often are reactive to symptomatic cases, they do not effectively control the disease. This is a question now being studied by the NAMRU-6 research team."

Morrison went on to say, this study is one of the first to generate this type of data in a developing country where dengue is endemic. The study suggests models that ignore differences in mobility due to fever could overestimate the potential for a disease to become pandemic.

NAMRU-6 Executive Officer, Cmdr. Guillermo Pimentel, explained, "This dengue study is another example of the contribution the NAMRU OCONUS (overseas) research laboratories make in generating products and new infectious disease knowledge for Global Health. Accurate disease forecasting and prediction models are crucial to understand and prevent epidemics of public health concerns."

Dengue is a mosquito-borne viral disease transmitted by female mosquitoes of the species *Aedes aegypti*. There are 4 distinct, but closely related, serotypes of the dengue virus. NAMRU-6 researchers have been studying dengue in Iquitos since 1990. They have characterized the invasion of serotype 1 in 1990, serotype 2 (American genotype) in 1995, serotype 3 in 2001, serotype 4 in 2008, and serotype 2 (Asian American genotype) in 2016. Researchers also added the Zika virus in May 2016.

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